

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:15:05 ; Search time 29.0579 seconds
(without alignments)
350.688 Million cell updates/sec

Title: US-09-893-615-89

Perfect score: 556

Sequence: 1 QIVLSQSPALLSASPGKVT.....COOWSSNPPTFGGTMLEIR 106

Scoring table:

BIOSUM62
GAPOP 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	94.1	106	2	PL0082
2	492	88.5	107	2	A42848
3	480	86.3	107	2	PC4405
4	474	85.3	107	2	A30562
5	473	85.1	105	2	S26338
6	469	84.4	107	2	B30562
7	466.5	83.9	108	2	G30560
8	465.5	83.7	108	2	S38720
9	462	83.1	140	2	PL0013
10	459	82.6	106	2	PS0071
11	458	82.4	104	2	BA9049
12	458	82.4	107	2	PL0011
13	458	82.4	130	1	JL0079
14	457	82.2	103	2	S29591
15	454	81.7	100	2	S29590
16	454	81.7	107	2	PT0406
17	452	81.3	97	2	S26341
18	446	80.2	106	2	B54378
19	445	80.0	235	2	S25058
20	444	79.9	107	2	S11118
21	442.5	79.6	104	2	JC6076
22	442	79.5	107	2	S11119
23	440	79.1	130	2	A32513
24	437	78.6	97	2	PH1084
25	434	78.1	107	2	S11121
26	433	77.9	107	2	S11117
27	433	77.9	130	2	B32456
28	433	77.9	130	2	S04573
29	430	77.3	99	2	S29585

30	429	77.2	106	2	G27887	Ig kappa chain V r
31	427	76.8	97	2	PH1085	Ig light chain V r
32	426	76.6	99	2	S26340	Ig light chain V r
33	426	76.6	99	2	D38601	Ig kappa chain V r
34	425	76.4	109	2	PT0405	Ig light chain V r
35	423	76.1	95	2	D33730	Ig kappa chain V r
36	423	76.1	107	2	S11112	Ig kappa chain V r
37	423	76.1	107	2	S29581	Ig kappa chain V r
38	423	76.1	108	2	PL0278	Ig kappa chain V r
39	421	75.7	108	2	PT0404	Ig light chain V r
40	420	75.5	109	2	S05268	Ig kappa chain pre
41	420	75.5	132	2	PS0070	Ig kappa chain V r
42	419	75.4	106	2	PS0070	Ig kappa chain V r
43	418	75.2	107	1	KVMSX4	Ig kappa chain V r
44	417	75.0	108	2	PL0276	Ig kappa chain V r
45	417	75.0	108	2	PL0277	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PL0082

Ig kappa chain V region (2D3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence:revision 07-Jun-1990 #text:change 21-Jan-2000

C:Accession: PL0082

R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brail, M.; Slaoui, M.; Urbain, J. Exp. Med. 169, 519-533, 1989

A:Title: Structural characterization of antidiabetic antibodies: evidence that Ab.

A:Reference number: PL0080; MUID:89094248; PMID:2492056

A:Accession: PL0082

A:Molecule type: mRNA

A:Residues: 1-106 <ME>

A:Experimental source: strain BALB/c

A:Note: The sequence shown here is from the V kappa region of an antidiabetic mon

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterodimer; immunoglobulin

F:16-89/Domain: Immunoglobulin homology <IMM>

Query Match 94.1%; Score 523; DB 2; Length 106;
Best Local Similarity 94.1%; Pred. No. 9, 2e-38;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps

QY 1 QIVLSQSPALLSASPGKVTMTGRASSVYMWYQKPGSSPKPVISATSNLASGVPAR 60
DB 1 QIVLSQSPALLSASPGKVTMTGRASSVYMWYQKPGSSPKPVISATSNLASGVPAR 60
QY 61 FSGSGSGTSTLTISRVEADATYCCQOWSSNPPTFGGTMLEIR 106
DB 61 FSGSGSGTSTLTISRVEADATYCCQOWSSNPPTFGGTMLEIR 106

RESULT 2

A42848

Ig light chain V region - mouse (fragment)

N:Alternate names: I6 anti-tumor antibody

C:Species: Mus musculus (house mouse)

C:Date: 27-Apr-1993 #sequence:revision 18-Nov-1994 #text:change 21-Jan-2000

C:Accession: A42848; S31902

R:Feil, H.P.; Gayle, M.A.; Yellon, D.; Lipsich, L.; Schayen, G.L.; Marken, J. Biol. Chem. 267, 15552-15558, 1992

A:Title: Chimeric I6 anti-tumor antibody: Genomic construction, expression, and cl

A:Reference number: A42848; MUID:92348410; PMID:1639754

A:Accession: A42848

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <FE>

A:Cross-references: EMBL:M00690

A:Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBI:109959)

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: immunoglobulin

F:16-89/Domain: Immunoglobulin homology <IMM>